

SEQUENCE LISTING

<110> UNO, Yumiko
 HIKICHI, Yukiko
 SAGIYA, Yoji
 NAKANISHI, Atsushi

<120> Novel Protein and its DNA

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<140> US 10/501,566

<141> 2004-07-15

<150> PCT/JP03/00311

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aaaaagaact	caggttgcac	agaagtctgc	catacgagga	aatcgacttc	ttccagagag	1020
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Pro Trp Gly Ile Ala Val Gly Leu Leu Cys Gln Phe Gly Leu Met Pro
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Phe Thr Ala Tyr Leu Leu Ala Ile Ser Phe Ser Leu Lys Pro Val Gln
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Asn Val Phe Thr Phe Trp Val Asp Gly Asp Met Asp Leu Ser Ile Ser
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      130     135     140
Ile Tyr Leu Tyr Thr Trp Ser Trp Ser Leu Gln Gln Asn Leu Thr Ile
      145     150     155     160
Pro Tyr Gln Asn Ile Gly Ile Thr Leu Val Cys Leu Thr Ile Pro Val
      165     170     175
Ala Phe Gly Val Tyr Val Asn Tyr Arg Trp Pro Lys Gln Ser Lys Ile
      180     185     190
Ile Leu Lys Ile Gly Ala Val Val Gly Gly Val Leu Leu Val Val
      195     200     205
Ala Val Ala Gly Val Val Leu Ala Lys Gly Ser Trp Asn Ser Asp Ile
      210     215     220
Thr Leu Leu Thr Ile Ser Phe Ile Phe Pro Leu Ile Gly His Val Thr
      225     230     235     240
Gly Phe Leu Leu Ala Leu Phe Thr His Gln Ser Trp Gln Arg Cys Arg
      245     250     255
Thr Ile Ser Leu Glu Thr Gly Ala Gln Asn Ile Gln Met Cys Ile Thr
      260     265     270
Met Leu Gln Leu Ser Phe Thr Ala Glu His Leu Val Gln Met Leu Ser
      275     280     285
Phe Pro Leu Ala Tyr Gly Leu Phe Gln Leu Ile Asp Gly Phe Leu Ile
      290     295     300
Val Ala Ala Tyr Gln Thr Tyr Lys Arg Arg Leu Lys Asn Lys His Gly
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Lys Lys Asn Ser Gly Cys Thr Glu Val Cys His Thr Arg Lys Ser Thr
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Ser Ser Arg Glu Thr Asn Ala Phe Leu Glu Val Asn Glu Glu Gly Ala

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 Ala Ser Ser Glu Pro Glu Glu Gly Ile Ser Val Phe Glu Leu Asp Tyr
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 Asp Tyr Val Gln Ile Pro Tyr Glu Val Thr Leu Trp Ile Leu Leu Ala
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 Ser Leu Ala Lys Ile Gly Phe His Leu Tyr His Arg Leu Pro Gly Leu
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Val	Ala	Val	Leu	Ala	Val	Phe	Glu	Glu	Ala	Arg	Val	Asn	Glu	Gln	Leu		
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Leu	Met	Asp	His	Leu	Lys	Ala	Gly	Ile	Glu	Asp	Val	Cys	Gly	His	Trp		
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Leu	Arg	Lys	Ile	Leu	Ile	Arg	Lys	Asn	Leu	Pro	Lys	Ser	Ser	Ile	Val		
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Ser	Leu	Tyr	Lys	Lys	Leu	Glu	Met	Lys	Gln	Ala	Ile	Glu	Met	Val	Glu		

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Arg Ile Gln Gly Ile Lys Arg Leu Ser	Pro Glu Asp Val Glu Ser Ile					
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Arg Asp Ile Leu Thr Ser Asn Met Tyr Gln Val Arg Gln Arg Thr Leu						
	595	600		605		
Ser Tyr Asn Lys Tyr Asn Leu Lys Pro Gln Thr Ser Glu Lys Gln Ala						
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Lys Gly His Ser Leu Pro Trp Gly Lys Pro Ala Gly Thr Lys Asn Ile						
	645	650		655		
Arg Tyr Leu Ser Tyr Pro Tyr Gly Asn Pro Gln Ser Ala Gly Arg Asp						
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Thr Arg Ala Ala Gly Phe Ser Asp Asp Asp Ser Ser Asp Pro Gly Ser						
	675	680		685		
Pro Ser Ile Thr Phe Ser Ala Cys Ser Arg Ile Gly Ser Leu Gln Lys						
	690	695		700		
Gln Glu Ala Gln Glu Ile Ile Pro Met Lys Ser Leu His Arg Gly Arg						
	705	710		715		720
Lys Ala Phe Ser Phe Gly Tyr Gln Arg Asn Thr Ser Gln Glu Glu Tyr						
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Leu Gly Gly Val Arg Arg Val Ala Leu Arg Pro Lys Pro Leu Phe His						
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Ala Val Asp Glu Glu Gly Glu Ser Gly Gly Glu Ser Glu Gly Lys Ala						
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		755					760					765									
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<212> DNA
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<212> DNA

<213> Human

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<223> Primer

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20

<210> 65

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe

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28

<210> 66

<211> 791

<212> PRT

<213> Human

<400> 66

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245	250	255
Glu Gly Phe Tyr Phe	Gly Glu Thr Pro Leu Ala	Leu Ala Ala Cys Thr
260	265	270
Asn Gln Pro Glu Ile Val	Gln Leu Leu Met Glu His	Glu Gln Thr Asp
275	280	285
Ile Thr Ser Arg Asp	Ser Arg Gly Asn Asn Ile	Leu His Ala Leu Val
290	295	300
Thr Val Ala Glu Asp	Phe Lys Thr Gln Asn Asp	Phe Val Lys Arg Met
305	310	315
Tyr Asp Met Ile Leu	Leu Arg Ser Gly Asn Trp	Glu Leu Glu Thr Thr
325	330	335
Arg Asn Asn Asp Gly	Leu Thr Pro Leu Gln Leu	Ala Ala Lys Met Gly
340	345	350
Lys Ala Glu Ile Leu	Lys Tyr Ile Leu Ser Arg	Glu Ile Lys Glu Lys
355	360	365
Arg Leu Arg Ser Leu	Ser Arg Lys Phe Thr Asp	Trp Ala Tyr Gly Pro
370	375	380
Val Ser Ser Ser Leu	Tyr Asp Leu Thr Asn Val	Asp Thr Thr Thr Asp
385	390	395
Asn Ser Val Leu Glu	Ile Thr Val Tyr Asn Thr	Asn Ile Asp Asn Arg
405	410	415
His Glu Met Leu Thr	Leu Glu Pro Leu His Thr	Leu Leu His Met Lys
420	425	430
Trp Lys Lys Phe Ala	Lys His Met Phe Phe Leu	Ser Phe Cys Phe Tyr
435	440	445
Phe Phe Tyr Asn Ile	Thr Leu Thr Leu Val Ser	Tyr Tyr Arg Pro Arg
450	455	460
Glu Glu Glu Ala Ile	Pro His Pro Leu Ala Leu	Thr His Lys Met Gly
465	470	475
Trp Leu Gln Leu Leu	Gly Arg Met Phe Val Leu	Ile Trp Ala Met Cys
485	490	495
Ile Ser Val Lys Glu	Gly Ile Ala Ile Phe Leu	Leu Arg Pro Ser Asp
500	505	510
Leu Gln Ser Ile Leu	Ser Asp Ala Trp Phe His	Phe Val Phe Phe Ile
515	520	525
Gln Ala Val Leu Val	Ile Leu Ser Val Phe Leu	Tyr Leu Phe Ala Tyr
530	535	540
Lys Glu Tyr Leu Ala	Cys Leu Val Leu Ala Met	Ala Leu Gly Trp Ala
545	550	555
Asn Met Leu Tyr Tyr	Thr Arg Gly Phe Gln Ser	Met Gly Met Tyr Ser
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Val Met Ile Gln Lys	Val Ile Leu His Asp Val	Leu Lys Phe Leu Phe
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Val Tyr Ile Val Phe	Leu Leu Gly Phe Gly Val	Ala Leu Ala Ser Leu
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Ile Glu Lys Cys Pro	Lys Asp Asn Lys Asp Cys	Ser Ser Tyr Gly Ser
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Phe Ser Asp Ala Val	Leu Glu Leu Phe Lys Leu	Thr Ile Gly Leu Gly
625	630	635
Asp Leu Asn Ile Gln	Gln Asn Ser Lys Tyr Pro	Ile Leu Phe Leu Phe
645	650	655
Leu Leu Ile Thr Tyr	Val Ile Leu Thr Phe Val	Leu Leu Leu Asn Met
660	665	670

Leu Ile Ala Leu Met Gly Glu Thr Val Glu Asn Val Ser Lys Glu Ser
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 Glu Arg Ile Trp Arg Leu Gln Arg Ala Arg Thr Ile Leu Glu Phe Glu
 690 695 700
 Lys Met Leu Pro Glu Trp Leu Arg Ser Arg Phe Arg Met Gly Glu Leu
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 Cys Lys Val Ala Glu Asp Asp Phe Arg Leu Cys Leu Arg Ile Asn Glu
 725 730 735
 Val Lys Trp Thr Glu Trp Lys Thr His Val Ser Phe Leu Asn Glu Asp
 740 745 750
 Pro Gly Pro Val Arg Arg Thr Ala Asp Phe Asn Lys Ile Gln Asp Ser
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 Glu Phe Pro Glu Thr Ser Val
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 <211> 2373
 <212> DNA
 <213> Human

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<212> DNA

<213> Artificial Sequence

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<223> Primer

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<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

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<223> Primer

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<210> 76

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 76

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29

<210> 77

<211> 27

<212> DNA

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<223> Primer

<400> 77
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 <400> 79
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 <400> 81
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 <212> DNA
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 <400> 82
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<210> 83
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<400> 83
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<210> 84
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<210> 85
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24

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<400> 93

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<223> Primer

<400> 94

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<223> Primer

<400> 95

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19

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<223> Primer

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<211> 697

<212> DNA

<213> Human

<400> 97

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<210> 99
 <211> 586
 <212> DNA
 <213> Human

<400> 99						
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 <211> 307
 <212> DNA
 <213> Human

<400> 100						
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<210> 101
 <211> 156
 <212> DNA
 <213> Human

<400> 101						
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<210> 102

<211> 2376
 <212> DNA
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<400> 102

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 <212> DNA
 <213> Human

<400> 103

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 <211> 373
 <212> PRT
 <213> Mouse

<400> 104

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			20					25					30		
Leu	Phe	Thr	Val	Leu	Ser	Ala	Val	Met	Val	Gly	Leu	Val	Met	Phe	Ser
		35					40					45			
Phe	Gly	Cys	Ser	Val	Glu	Ser	Gln	Lys	Leu	Trp	Leu	His	Leu	Arg	Arg
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Pro	Trp	Gly	Ile	Ala	Val	Gly	Leu	Leu	Ser	Gln	Phe	Gly	Leu	Met	Pro
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			85					90						95	
Ala	Ile	Ala	Val	Leu	Met	Met	Gly	Ser	Cys	Pro	Gly	Gly	Thr	Ile	Ser
			100					105					110		
Asn	Val	Leu	Thr	Phe	Trp	Val	Asp	Gly	Asp	Met	Asp	Leu	Ser	Ile	Ser

115	120	125
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130	135	140
Leu Tyr Ile Tyr Thr Arg	Ser Trp Thr Leu Thr	Gln Asn Leu Val Ile
145	150	155
Pro Tyr Gln Ser Ile Gly	Ile Thr Leu Val Ser	Leu Val Val Pro Val
165	170	175
Ala Ser Gly Val Tyr Val	Asn Tyr Arg Trp Pro	Lys Gln Ala Thr Val
180	185	190
Ile Leu Lys Val Gly Ala	Ile Leu Gly Gly Met	Leu Leu Leu Val Val
195	200	205
Ala Val Thr Gly Met Val	Leu Ala Lys Gly Trp	Asn Thr Asp Val Thr
210	215	220
Leu Leu Val Ile Ser Cys	Ile Phe Pro Leu Val	Gly His Val Thr Gly
225	230	235
Phe Leu Leu Ala Phe Leu	Thr His Gln Ser Trp	Gln Arg Cys Arg Thr
245	250	255
Ile Ser Ile Glu Thr Gly	Ala Gln Asn Ile Gln	Leu Cys Ile Ala Met
260	265	270
Leu Gln Leu Ser Phe Ser	Ala Glu Tyr Leu Val	Gln Leu Leu Asn Phe
275	280	285
Ala Leu Ala Tyr Gly Leu	Phe Gln Val Leu His	Gly Leu Leu Ile Val
290	295	300
Ala Ala Tyr Gln Ala Tyr	Lys Arg Arg Gln Lys	Ser Lys Cys Arg Arg
305	310	315
Gln His Pro Asp Cys Pro	Asp Val Cys Tyr Glu	Lys Gln Pro Arg Glu
325	330	335
Thr Ser Ala Phe Leu Asp	Lys Gly Asp Glu Ala	Ala Val Thr Leu Gly
340	345	350
Pro Val Gln Pro Glu Gln	His His Arg Ala Ala	Glu Leu Thr Ser His
355	360	365
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370		

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 <212> DNA
 <213> Mouse

<400> 105

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<220>
 <223> Primer

<400> 106
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<210> 107
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<220>
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<400> 107
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<210> 108
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21

<210> 112
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26

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19

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 gtctgagagg atacagggaa tcaagcggct ttctcctgaa gacgtggagt ccatgcgagg 180
 cattctgaca agaagcatgt accaagttcg acaaagaacc ctatcctaca acaaatacaa 240
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 <400> 126
 ccggaggaac ctgccaaaat caa 23

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 <220>
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 <400> 127
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<210> 128
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 <220>
 <223> Primer

 <400> 128
 gatgaaacag gccattgaga tg 22

 <210> 129
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 <220>
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 <400> 129
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 <400> 130
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 cagtgacaat gaaaaagtac gtggaagaga acgtgtccca gacgtcgtac acgaccatca 240
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21

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35

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caaccatctg	gccgaccatc	cccattgtct	ctgacatgaa	agggcaggca	actatgggtcc	600
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<220>

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<210> 148
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<220>
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 aactatggtc ctgagttctg cccacttctg gttgggtttg ctcttggttc ccactgcgtg 660
 tttgatcgag gatgtggcgt ggagagcggc caaacacacc tgcaaaaaga cactgtcttg 720
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<210> 151
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<220>
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<400> 151
 accagaagtg ggcagaactc a 21

<210> 152

<211> 28
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<220>
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<400> 152
 catagttgcc tgccctttca tgtcagga 28

<210> 153
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<400> 153
 ttggatccgt cgacatgtcc cgggccacgt ctgttgg 37

<210> 154
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<220>
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<400> 154
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<210> 155
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 gtcgctgaag ctgccatagg aactg 25

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 <400> 158
 ctgagaccct ccgatcttca gt 22

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 <400> 160
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ctccacagtc tcgcccata g

21

<210> 170

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24

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23

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24